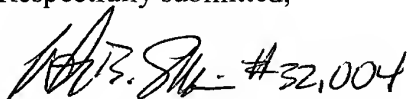


REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned "**Version With Markings to Show Changes Made**".

Respectfully submitted,



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FILED: 22 MARCH 2002

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 5, 8-9, 11-12, 14-17, 21, 25-26, 33 and 37 have been amended as follows:

5. (Amended) A method according to paragraph 1 wherein the reactions are determined over time and the resulting kinetic data is used to determine the reaction products.
8. (Amended) A method according to paragraph 1, wherein reactions of two or more indexing reagents with the population are multiplexed together.
9. (Amended) A method according to paragraph 1, wherein a substantial fraction of the possible sub-populations of a given type are thus determined.
11. (Amended) A method according to paragraph 9, wherein substantially all of the sub-population are determined.
12. (Amended) A method according to paragraph 1, wherein the population is a population of polynucleotides and the sub-populations are sequence-specific sub-populations.
14. (Amended) A method according to paragraph 12, wherein the population is a population of mRNAs.
15. (Amended) A method according to paragraph 12, wherein the population is a representative of mRNAs.
16. (Amended) A method according to paragraph 12, wherein the population is a population of cDNAs.
17. (Amended) A method according to paragraph 1, wherein the indexing reagents comprise sequence-specific indexing probes.

21. (Amended) A method according to 17, wherein the sequence-specific probe is n bases long, each different sequence possible for a sequence n bases long is specific for a sub-population to be determined, and indexing reactions between the population and indexing reagents that comprise a substantial fraction of all the possible sequences n bases long are determined.
25. (Amended) A method according to paragraph 1, wherein the indexing reagents comprise amplification primers.
26. (Amended) A method according to paragraph 1, wherein the probes are stand-d is placement indexing adaptors.
33. (Amended) A device according to 29, wherein the indexing reagents comprise sequence-specific indexing probes.
37. (Amended) A device according to paragraph 29, wherein the sequence-specific probe is n bases long, each different sequence possible for a sequence n bases long is specific for a sub-population to be determined, and the plurality of indexing reagents comprise indexing reagents with a substantial fraction of all the possible sequences n bases long.